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ERROR DETEC SUGGESTED CORRECTION SERIAL NUMBER: 09/674,195

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 _____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 _____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 _____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 _____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 _____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 _____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
8 _____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 _____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 _____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 _____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 _____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 _____	PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT09

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195 TIME: 17:17:37

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Output Set: N:\CRF3\01112001\I674195.raw

<110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
DEPARTMENT OF HEALTH AND HUMAN SERVICES CENTERS FOR DISEASE CONTROL AND
PREVENTION
ZANCOPE-OLIVEIRA, ROSALY M.
LOTT, TIMOTHY J.
MAYER, LEONARD W.
REISS, ERROL
DEEPE, JR., GEORGE S.
<120> TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
HISTOPLASMA CAPSULATUM, ISOLATED AND RECOMBINANTLY-PRODUCED
ANTIGENS, VACCINES AND ANTIBODIES, METHODS AND KITS FOR
DETECTING HISTOPLASMOSIS
<130> FILE REFERENCE: 65798 / US
<140> CURRENT APPLICATION NUMBER: US/09/674,195
<141> CURRENT FILING DATE: 2000-10-26
<150> PRIOR APPLICATION NUMBER: U.S. 60/083,676
<151> PRIOR FILING DATE: 1998-04-30
<150> PRIOR APPLICATION NUMBER: PCT/US99/09151
<151> PRIOR FILING DATE: 1999-04-27
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PATENT APPLICATION: US/09/674,195 TIME: 17:17:37

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    108 <212> TYPE: PRT
    109 <213> ORGANISM: Histoplasma capsulatum
    111 <400> SEQUENCE: 2
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→ see item 10 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195 TIME: 17:17:37

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Output Set: N:\CRF3\01112001\I674195.raw

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115              20                  25                  30
116  Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
117          35                  40                  45
118  Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
119      50                  55                  60
120  Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
121  65                  70                  75                  80
122  Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
123                  85                  90                  95
124  Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
125              100                 105                 110
126  Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
127          115                 120                 125
128  Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
129      130                 135                 140
130  Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
131  145                 150                 155                 160
132  Phe Phe Ile Glu Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
133                  165                 170                 175
134  Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
135              180                 185                 190
136  Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
137          195                 200                 205
138  Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
139      210                 215                 220
140  Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
141  225                 230                 235                 240
142  Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
143                  245                 250                 255
144  Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
145              260                 265                 270
146  His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
147          275                 280                 285
148  Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
149      290                 295                 300
150  Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
151  305                 310                 315                 320
152  Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
153                  325                 330                 335
154  Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
155              340                 345                 350
156  Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
157          355                 360                 365
158  Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
159      370                 375                 380
160  Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
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RAW SEQUENCE LISTING DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195 TIME: 17:17:37

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Output Set: N:\CRF3\01112001\I674195.raw

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166  Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
167          435                 440                 445
168  Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
169      450                 455                 460
170  Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
171  465                 470                 475                 480
172  Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
173                  485                 490                 495
174  Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
175              500                 505                 510
176  Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
177          515                 520                 525
178  Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
179      530                 535                 540
180  Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
181  545                 550                 555                 560
182  Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
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184  Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
185              580                 585                 590
186  Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
187          595                 600                 605
188  Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
189      610                 615                 620
190  Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
191  625                 630                 635                 640
192  Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
193                  645                 650                 655
194  Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
195              660                 665                 670
196  Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
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200  Ser
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204 <211> LENGTH: 8
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RAW SEQUENCE LISTING DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195 TIME: 17:17:37

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<210> SEQ ID NO: 10
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VERIFICATION SUMMARY DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195 TIME: 17:17:38

Input Set : A:\65798 10_27_00.TXT
Output Set: N:\CRF3\01112001\I674195.raw

L:21 M:270 C: Current Application Number differs, Replaced Current Application Number
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:94 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:94 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
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L:94 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
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L:286 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION **SERIAL NUMBER:** 09/674,195

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.